SEP 25 700 H

SEQUENCE LISTING

<110> Kubin, Marek Z.
 Goodwin, Raymond G.

- <120> NK Cell Activation Inducing Ligand (NAIL) DNA and Polypeptides, and Uses Thereof
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- <140> 09/667,859
- <141> 2000-09-20
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Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His 50 55 60

His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn 65 70 75 80

Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala 85 90 95

Ala Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile
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Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val 145 150 155 160

Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn 165 170 175

Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr 180 185 190

Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn 195 200 205

Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Phe Trp Pro 210 215 220

225 230 235 Ala Cys Phe Cys Val Trp Arg Arg Lys Arg Lys Glu Lys Gln Ser Glu Thr Ser Pro Lys Glu Phe Leu Thr Ile Tyr Glu Asp Val Lys Asp Leu 265 Lys Thr Arg Arg Asn His Glu Gln Glu Gln Thr Phe Pro Gly Gly Gly Ser Thr Ile Tyr Ser Met Ile Gln Ser Gln Ser Ser Ala Pro Thr Ser 295 300 Gln Glu Pro Ala Tyr Thr Leu Tyr Ser Leu Ile Gln Pro Ser Arg Lys 305 Ser Gly Ser Arg Lys Arg Asn His Ser Pro Ser Phe Asn Ser Thr Ile Tyr Glu Val Ile Gly Lys Ser Gln Pro Lys Ala Gln Asn Pro Ala Arg Leu Ser Arg Lys Glu Leu Glu Asn Phe Asp Val Tyr Ser <210> <211> 2440 <212> DNA <213> Homo sapiens <400> eggeettgte ageteacage aggegttaac ageetetaat tgaggaaact gtggetggae 60 aggttgcaag gcagttctgc tccccatcgt cctcttgctg actggggact gctgagcccg 120 tgcacggcag agagtctggt ggggtggagg ggctggcctg gcccctctgt cctgtggaaa 180 tgctggggca agtggtcacc ctcatactcc tcctgctcct caaggtgtat cagggcaaag 240 gatgccaggg atcagctgac catgtggtta gcatctcggg agtgcctctt cagttacaac 300 caaacagcat acagacgaag gttgacagca ttgcatggaa gaagttgctg ccctcacaaa 360 atggatttca tcacatattg aagtgggaga atggctcttt gccttccaat acttccaatg 420 atagattcag ttttatagtc aagaacttga gtcttctcat caaggcagct cagcagcagg 480 acagtggcct ctactgcctg gaggtcacca gtatatctgg aaaagttcag acagccacgt 540 tccaggtttt tgtatttgat aaagttgaga aaccccgcct acaggggcag gggaagatcc 600

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Val Ser Val Gln Trp Lys Lys Thr Glu Gln Gly Ser His Arg Lys Ile 50 60

Glu Ile Leu Asn Trp Tyr Asn Asp Gly Pro Ser Trp Ser Asn Val Ser 65 70 75 80

Phe Ser Asp Ile Tyr Gly Phe Asp Tyr Gly Asp Phe Ala Leu Ser Ile 85 90 95

Lys Ser Ala Lys Leu Gln Asp Ser Gly His Tyr Leu Leu Glu Ile Thr 100 105 110

Asn Thr Gly Gly Lys Val Cys Asn Lys Asn Phe Gln Leu Leu Ile Leu 115 120 125

Asp His Val Glu Thr Pro Asn Leu Lys Ala Gln Trp Lys Pro Trp Thr 130 135 140

Asn Gly Thr Cys Gln Leu Phe Leu Ser Cys Leu Val Thr Lys Asp Asp 145 150 155 160

Asn Val Ser Tyr Ala Phe Trp Tyr Arg Gly Ser Thr Leu Ile Ser Asn 165 170 175

Gln Arg Asn Ser Thr His Trp Glu Asn Gln Ile Asp Ala Ser Ser Leu 180 185 190

His Thr Tyr Thr Cys Asn Val Ser Asn Arg Ala Ser Trp Ala Asn His 195 200 205

Thr Leu Asn Phe Thr His Gly Cys Gln Ser Val Pro Ser Asn Phe Arg 210 215 220

Gly Ala Ile Ile Cys Phe Cys Val Trp Thr Lys Lys Arg Lys Gln Leu Gln Phe Ser Pro Lys Glu Pro Leu Thr Ile Tyr Glu Tyr Val Lys Asp 265 Ser Arg Ala Ser Arg Asp Gln Gln Gly Cys Ser Arg Ala Ser Gly Ser Pro Ser Ala Val Gln Glu Asp Gly Arg Gly Gln Arg Glu Leu Asp Arg 290 295 300 Arg Val Ser Glu Val Leu Glu Gln Leu Pro Gln Gln Thr Phe Pro Gly 305 Asp Arg Gly Thr Met Tyr Ser Met Ile Gln Cys Lys Pro Ser Asp Ser Thr Ser Gln Glu Lys Cys Thr Val Tyr Ser Val Val Gln Pro Ser Arg Lys Ser Gly Ser Lys Lys Arg Asn Gln Asn Tyr Ser Leu Ser Cys Thr 355 Val Tyr Glu Glu Val Gly Asn Pro Trp Leu Lys Ala His Asn Pro Ala 370 375 380 Arg Leu Ser Arg Arg Glu Leu Glu Asn Phe Asp Val Tyr Ser 385 <210> 5 <211> 1147 <212> DNA <213> Mus musculus atgttggggc aagctgteet gtteacaace tteetgetee teagggetea teagggeeaa 60 gactgcccag attcttctga agaagtggtt ggtgtctcag gaaagcctgt ccagctgagg 120 ccttccaaca tacagacaaa agatgtttct gttcaatgga agaagacaga acagggctca 180 cacagaaaaa ttgagatcct gaattggtat aatgatggtc ccagttggtc aaatgtatct 240 tttagtgata tctatggttt tgattatggg gattttgctc ttagtatcaa gtcagctaag 300 ctgcaagaca gtggtcacta cctgctggag atcaccaaca caggcggaaa agtgtgcaat 360

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Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His 50 60

His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn 65 70 75 80

Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala 85 90 95

Ala Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile 100 105 110

Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys 115 120 125

Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly 130 135 140

Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val 145 150 155 160

Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn 165 170 175

Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr 180 185 190

Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn 195 200 205

Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Arg Ser Cys 210 220

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly 225 230 235 240

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met 245 250 255

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
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Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val 275 280 285

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Ser Gly Val Pro Leu Gln Leu Gln Pro Asn Ser Ile Gln Thr Lys Val 35 40 45

Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His 50 55 60

His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn 65 70 75 80

Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala 85 90 95

Ala Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile 100 105 110

Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys 115 120 125

Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly 130 135 140

Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val 145 150 155 160

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Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn 195 200 205

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Asp Ser Ile Ala Trp Lys Lys Leu Leu Pro Ser Gln Asn Gly Phe His 50 55 60

His Ile Leu Lys Trp Glu Asn Gly Ser Leu Pro Ser Asn Thr Ser Asn 65 70 75 80

Asp Arg Phe Ser Phe Ile Val Lys Asn Leu Ser Leu Leu Ile Lys Ala 85 90 95

Ala Gln Gln Asp Ser Gly Leu Tyr Cys Leu Glu Val Thr Ser Ile 100 $$ 105 $$ 110

Ser Gly Lys Val Gln Thr Ala Thr Phe Gln Val Phe Val Phe Asp Lys
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Val Glu Lys Pro Arg Leu Gln Gly Gln Gly Lys Ile Leu Asp Arg Gly 130 135 140

Arg Cys Gln Val Ala Leu Ser Cys Leu Val Ser Arg Asp Gly Asn Val 145 150 155 160

Ser Tyr Ala Trp Tyr Arg Gly Ser Lys Leu Ile Gln Thr Ala Gly Asn 165 170 175

Leu Thr Tyr Leu Asp Glu Glu Val Asp Ile Asn Gly Thr His Thr Tyr 180 185 190

Thr Cys Asn Val Ser Asn Pro Val Ser Trp Glu Ser His Thr Leu Asn 195 200 205

Leu Thr Gln Asp Cys Gln Asn Ala His Gln Glu Phe Arg Arg Ser Gly 210 215 220

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Leu Pro Glu Asn Tyr Lys Gln Leu Thr Trp Phe Tyr Thr Phe Asp Gln 50 55 60

Lys Ile Val Glu Trp Asp Ser Arg Lys Ser Lys Tyr Phe Glu Ser Lys 65 70 75 80

Phe Lys Gly Arg Val Arg Leu Asp Pro Gln Ser Gly Ala Leu Tyr Ile 85 90 95

Ser Lys Val Gln Lys Glu Asp Asn Ser Thr Tyr Ile Met Arg Val Leu 100 105 110

Lys Lys Thr Gly Asn Glu Gln Glu Trp Lys Ile Lys Leu Gln Val Leu 115 120 125

Asp Pro Val Pro Lys Pro Val Ile Lys Ile Glu Lys Ile Glu Asp Met 130 140

Asp Asp Asn Cys Tyr Leu Lys Leu Ser Cys Val Ile Pro Gly Glu Ser 145 150 155

Val Asn Tyr Thr Trp Tyr Gly Asp Lys Arg Pro Phe Pro Lys Glu Leu 165 170 175

Gln Asn Ser Val Leu Glu Thr Thr Leu Met Pro His Asn Tyr Ser Arg 180 185 190

Cys Tyr Thr Cys Gln Val Ser Asn Ser Val Ser Ser Lys Asn Gly Thr 195 200 205

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